A vision for development and utilization of high-throughput phenotyping and big data analytics in livestock

James E. Koltes[1*], John B. Cole[2], Roxanne Clemmens[3], Ryan N. Dilger[4], Luke M. Kramer[1], Joan K. Lunney[5], Molly E. McCue[6], Stephanie McKay[7], Raluca Mateescu[8], Brenda M. Murdoch[9], Ryan Reuter[10], Caird Rexroad[11], Guilherme J. Rosa[12], Nick V. Serão[1], Stephen N. White[13, 14, 15], Mary J. Woodward-Greene[11], Millie Worku[16], Hongwei Zhang[17], James Reecy[1*]

[1]Department of Animal Science, College of Agriculture and Life Sciences, Iowa State University, United States, [2]Animal Genomics and Improvement Laboratory (USDA-ARS), United States, [3]College of Agriculture and Life Sciences, Iowa State University, United States, [4]Department of Animal Sciences, University of Illinois at Urbana-Champaign, United States, [5]Animal Parasitic Diseases Laboratory, United States Department of Agriculture, Agricultural Research Service, United States, [6]Department of Veterinary Population Medicine, College of Veterinary Medicine, University of Minnesota, United States, [7]Department of Animal and Veterinary Sciences, College of Agriculture and Life Sciences, University of Vermont, United States, [8]Department of Animal Sciences, University of Florida, United States, [9]University of Idaho, United States, [10]Department of Animal & Food Sciences, College of Agricultural Sciences & Natural Resources, Oklahoma State University, United States, [11]Agricultural Research Service, United States Department of Agriculture, United States, [12]Department of Dairy Science, University of Wisconsin-Madison, United States, [13]Animal Disease Research Unit, Agricultural Research Service, United States Department of Agriculture, United States, [14]Department of Veterinary Microbiology and Pathology, College of Veterinary Medicine, Washington State University, United States, [15]Center for Reproductive Biology, College of Veterinary Medicine, Washington State University, United States, [16]North Carolina Agricultural and Technical State University, United States, [17]Department of Electrical and Computer Engineering, College of Engineering, Iowa State University, United States

Submitted to Journal:
Frontiers in Genetics

Specialty Section:
Livestock Genomics

Article type:
Review Article

Manuscript ID:
480865

Received on:
26 Jun 2019

Frontiers website link:
www.frontiersin.org

Conflict of interest statement

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest

Author contribution statement

All authors participated in the meeting and helped write the paper.

Keywords

High-throughput phenotyping (HTP), Sensors, big-data analytics, Phenomics, precision agriculture

Abstract

Word count: 216

Automated high-throughput phenotyping with sensors, imaging, and other on-farm technologies has resulted in a flood of data that are largely under-utilized. Drastic cost reductions in sequencing and other omics technology have also facilitated the ability for deep phenotyping of livestock at the molecular level. These advances have brought the animal sciences to a cross-roads in data science where increased training is needed to manage, record, and analyze data to generate knowledge and advances in agriscience related disciplines. This paper describes the opportunities and challenges in using high-throughput phenotyping, "big data," analytics, and related technologies in the livestock industry based on discussions at the Livestock High-Throughput Phenotyping and Big Data Analytics meeting, held in November 2017 (see: https://www.animalgenome.org/bioinfo/community/workshops/2017/). Critical needs for investments in infrastructure for people (e.g. "big data" training), data (e.g. data transfer, management and analytics), and technology (e.g. development of low cost sensors) were defined by this group. Though some subgroups of animal science have extensive experience in predictive modeling, cross-training in computer science, statistics and related disciplines are needed to use big data for diverse applications in the field. Extensive opportunities exist for public and private entities to harness big data to develop valuable research knowledge and products to the benefit of society under the increased demands for food of a rapidly growing population.

Contribution to the field

This manuscript describes priorities set by scientists from a variety of disciplines gathered at USDA in Beltsville, MD to discuss the potential of big data, high-throughput phenotyping and precision agriculture technologies to transform animal agriculture in the US. Our meeting was entitled the, "Livestock High-Throughput Phenotyping and Big Data Analytics (Livestock HTP and Big Data) meeting," https://www.animalgenome.org/share/meetings/LivestockHTP This meeting brought together industry, academia, government and funding agency representatives to discuss benefits and challenges in establishing analytics, technologies and expertise to utilize the wealth of high-throughput data generated in animal agriculture. Animal scientists, engineers, computer scientists and statisticians interacted in these discussions to set research priorities for funding agencies. This manuscript describes the investments needed in data, technologies and people this consortium felt were important in precision livestock science. It serves as a road map, including background examples of data science in the animal sciences, standardized terminology, guidelines for data management and the concept of a data driven triad in livestock big data analysis focused on technology, data and people centered around animals. Though there are other manuscripts on the application of precision data in livestock, this manuscript stands alone as a benchmark on research priorities defined by academia and industry.

Funding statement

This meeting was supported by a competitive USDA-NIFA grant # 2017-67015-26907

Data availability statement

Generated Statement: No datasets were generated or analyzed for this study.